Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

Claims 1-18 (cancelled)

19. (New) A method for generating a secondary library of protein variants of a target protein comprising:

a) inputting the coordinates of said target protein into a computer;

b) utilizing a scoring function to generate a filtered set of optimized primary variant sequences;

c) computationally generating a probability distribution table of variant amino acid residues in a plurality of said primary variant positions from said filtered set of optimized primary variant sequences; and,

d) combining a plurality of said variant amino acid residues to generate a secondary library of secondary variant proteins, wherein at least one of said secondary variant proteins is different from said optimized primary protein sequences..

20. (New) A method according to claim 19, further comprising synthesizing a plurality of said secondary variant proteins wherein said combining comprises:

a) generating a set of oligonucleotide probes each encoding at least one of said variant amino acid residues;

b) using said probes in a polymerase chain reaction (PCR) to generate a plurality of oligonucleotide sequences, each encoding at least one of said secondary variant proteins; and,

c) producing said secondary variant proteins in host cells transformed with said oligonucleotide sequences.

21. (New) A method according to claim 19, wherein said scoring function is selected from the group consisting of a van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function

22. (New) A method for generating a tertiary library of scaffold protein variants comprising:

a) utilizing Protein Design Automation (PDA®) to computationally generating a primary library of scaffold protein primary variant sequences ;

b) generating a list of primary variant positions in said primary library;

c) combining a plurality of said primary variant positions to generate a secondary library of secondary sequences;

d) synthesizing a plurality of tertiary library variant protein sequences by recombining said library of secondary sequences, wherein at least one of said tertiary variants is different from said primary and secondary variants; and,

e) screening said tertiary library protein sequences for a desired protein property.

23. (New) A method according to claim 22 wherein said generating of said primary variant positions is by using a probability distribution table.

24. (New) A method according to claim 22 wherein said combining of said primary variant positions is by using a probability distribution table.

25. (New) A method according to claim 22, wherein said list is a rank-ordered list.

26. (New) A method according to claim 22 wherein said recombining is done computationally.

27. (New) A method according to claim 22 wherein said recombining is done experimentally.

28. (New) A method according to claim 22 wherein said recombining is done by gene shuffling.

29. (New) A method according to claim 22 wherein said recombining is done by multiple PCR with pooled oligonucleotides.

30. (New) A method for generating a secondary library of protein variants of a target protein, the method comprising:

transmitting coordinates for a three-dimensional target protein backbone structure with variable residue positions to a microprocessor configured to establish a group of potential amino acids for each of said variable residue, including providing instructions to generate a secondary library of secondary sequences, said instructions comprising:

a) utilizing PDA® to generate a primary library comprising a filtered set of optimized primary variant sequences; and,

b) computationally generating a probability distribution table of variant amino acid residues in a plurality of said primary variant positions from said filtered set of optimized primary variant sequences; and,

c) combining a plurality of said variant amino acid residues to generate a secondary library of protein variants.

31. (New) A method according to claim 30 wherein set filtered set of optimized primary variant sequences is generated using a ranking function.

32. (New) A method according to claim 30 wherein set filtered set of optimized primary variant sequences is generated using a ranking function.